Table S1 Primer sequences and characteristics of plastid DNA microsatellite loci in *Pitcairnia* spp., including locus name, plastid DNA region, primer sequences, repeat type, allele size range, and no. of alleles.

Table S2 Genetic variability at 15 microsatellite loci in *P. staminea*, *P. albiflos*, and their hybrids, including locus name, number of alleles (A), observed heterozygosity (H_O), expected heterozygosity (H_E), standardized measure of differentiation (G'_{ST}), fixation index (F_{ST}), total inbreeding coefficient (F_{IT}), and within-population inbreeding coefficient (F_{IS}).

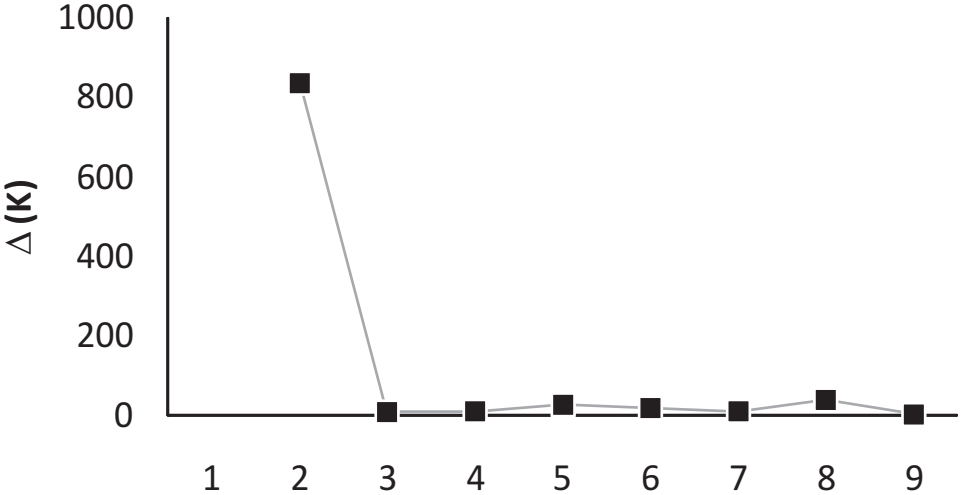
Table S3 Analysis of Molecular Variance (amova) based on nuclear microsatellite data for *P. staminea* and *P. albiflos* for two different hierarchical models. (A) species level. (B) geographical level (inland vs. coastal inselbergs). Percentages of variation in parentheses refer to models in which hybrids were nested with *P. albiflos*.

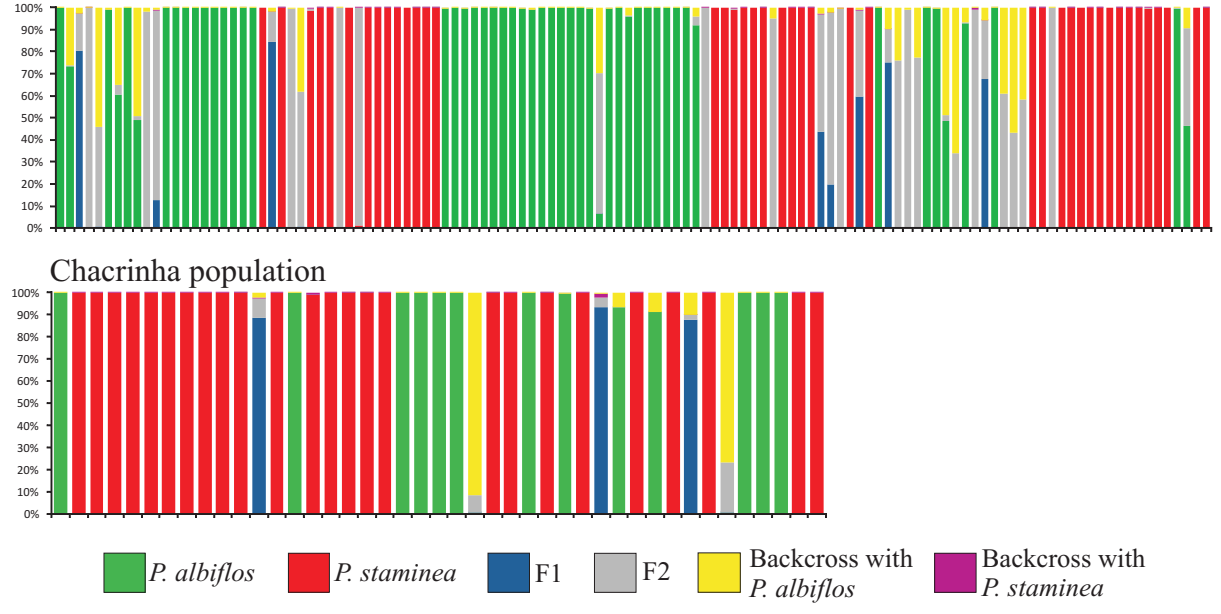
Table S4 Genetic divergence (F_{ST}; below diagonal) and gene flow (N_em; above diagonal) for pairs of populations of the inselberg bromeliads *Pitcairnia albiflos* and *P. staminea* and their hybrids. $N_em = (1/F_{ST} - 1)/4$.

Table S5 Locus-specific, bidirectional introgression rates between *Pitcairnia albiflos* and *P. staminea* on PAO population.

Fig. S1 Magnitude of ΔK from structure analysis as a function of K (mean ± SD over 10 replicates), calculated following the ΔK method proposed by Evanno *et al.* (2005), for *Pitcairnia albiflos* and *P. staminea* microsatellite data.

Fig. S2 Posterior probabilities (q) of *Pitcairnia albiflos* and *Pitcairnia staminea* for the two hybrid zones analyzed with newhybrids.


1000
800
600
400
200
0
Δ (K)
1
2
3
4
5
6
7
8
9


Pão de Açúcar population
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
Chacrinha population
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
P. albiflos
P. staminea
F1
F2
Backcross with P. albiflos
Backcross with P. staminea

Supplementary Figure 1 Magnitude of ΔK from STRUCTURE analysis as a function of K (mean ± s.d. over 10 replicates), calculated following the ΔK method proposed by Evanno *et al.* (2005), for *Pitcairnia albiflos* and *P. staminea* microsatellite data. The modal value of these distributions indicates the true *K* or the uppermost level of structure, here two 'genetic clusters' in agreement with the accepted morphological classification of these species.

Supplementary Figure 2 Posterior probabilities (*q*) of *Pitcairnia albiflos* and *Pitcairnia staminea* for the two hybrid zones analyzed with NEWHYBRIDS. The proportion of color in each bar represents an individual's assignment probability, according to different categories (pure parental species, hybrid F1, F2, and backcrosses).

Supplementary Table 1. Primer sequences and characteristics of plastid DNA microsatellite loci in *Pitcairnia* spp., including locus name, plastid DNA region, primer sequences, repeat type, allele size range, and no. of alleles.

Locus	Location	Primers (5'-3')	Repeat	Size (bp)	N° of alleles
[a] PaCP1	[1]rps16 – *trn*K	TTGCCTTGCTGCATTTACTC CGTTGAACTAGCAACACATCG	(T)6 G (T)3	196	3
[a] PaCP2	[2]trnD^{GUC}F^{-}trnT^{GGU}	TGCATAGGAGTTCATTCAGGA GGGCCTGTCTTGAAACAATTTA	(T)12	140	6
[a] PaCP3	[3] *trn*H^{GUG}– *psb*A	AGATGCCCGAGACCAAGTTA TCGAGATATTGGACATAGAATGC	(T)10	175	2
[a] PaCP4	[4]rpL16F71– rpL16R1516	CCAAGTAATGGCTTTTATTGAT GCCCGCGAAACCTTTATTTA	(T)9	222	3
[a] PaCP5	[5]trnT^{UGU}A – trnL^{UAA}B	TCTACCGATTTCGCCATATC GAAAATAGCAGCCTTTTCGAT	(T)8	111	3
[b] VgCP4	petG	ACCTACGACATCGGGTTTTG TTCTCCTATGGGCAGTAACGA	(A)5(T)9	186	4

[a] Plastid DNA microsatellite markers isolated *de novo* from *Pitcairnia albiflos* and *P. staminea*; [b] Marker isolated by Palma-Silva *et al.* (2009).
[1] Universal DNA sequencing primers used for identification of the markers, designed by Shaw *et al.* (2007); [2] Universal primers designed by Demesure *et al.* (1995); [3] Universal primers designed by Sang *et al.* (1997); [4] Universal primers designed by Small *et al.* (1998); [5]Universal primers designed by Taberlet *et al.* (1991).

Supplementary Table 2. Genetic variability at 15 microsatellite loci in *P. staminea*, *P. albiflos*, and their hybrids, including locus name, number of alleles (A), observed heterozygosity (H_O), expected heterozygosity (H_E), standardized measure of differentiation ($G`_{ST}$), fixation index (F_{ST}), total inbreeding coefficient (F_{IT}), and within-population inbreeding coefficient (F_{IS}).

	P. albiflos							***P. staminea***							**Hybrids**						
Locus	**A**	**H_O**	**H_E**	**$G`_{ST}$**	**F_{ST}**	**F_{IT}**	**F_{IS}**	**A**	**H_O**	**H_E**	**$G`_{ST}$**	**F_{ST}**	**F_{IT}**	**F_{IS}**	**A**	**H_O**	**H_E**	**$G`_{ST}$**	**F_{ST}**	**F_{IT}**	**F_{IS}**
pit5[a]	3	0.24	0.24	0.44	0.34	0.32	-0.03	2	0.15	0.14	0.35	0.34	0.27	0.23	3	0.14	0.13	-0.01	0.00	-0.02	-0.01
pit8[a]	4	0.26	0.34	0.58	0.43	0.18	0.29	4	0.09	0.21	0.10	0.10	0.66	0.48***	3	0.14	0.40	-0.06	-0.08	0.36	0.66*
pit9[a]	10	0.51	0.50	0.73	0.29	0.27	-0.04	11	0.50	0.61	0.72	0.30	0.51	0.17***	6	0.39	0.40	0.51	0.24	0.23	-0.02
E6b[b]	6	0.39	0.59	0.29	0.17	0.50	0.32**	5	0.29	0.36	0.14	0.08	0.30	0.15***	4	0.70	0.65	0.54	0.20	0.24	-0.09
ct5[b]	10	0.43	0.42	0.62	0.46	0.35	0.03	17	0.51	0.59	0.87	0.82	0.84	0.32	7	0.70	0.61	0.15	0.07	-0.06	-0.17
e19[b]	2	0.00	0.01	0.00	-0.02	0.43	1.00***	2	0.08	0.10	0.90	0.40	0.54	0.17***	2	0.00	0.04	-0.01	-0.11	1.00	1.00***
VgA04[c]	9	0.40	0.50	0.42	0.34	0.47	0.20**	8	0.46	0.51	0.69	0.34	0.55	0.18***	6	0.55	0.73	0.34	0.10	0.32	0.25*
PaA05[d]	8	0.45	0.45	0.90	0.46	0.52	0.00	9	0.53	0.60	0.54	0.21	0.37	0.20***	6	0.82	0.79	0.07	0.01	0.13	-0.06
PaA09[d]	18	0.63	0.71	0.79	0.24	0.31	0.11	16	0.56	0.64	0.47	0.18	0.33	0.13***	10	0.85	0.83	0.43	0.07	0.17	-0.05
PaA10[d]	3	0.39	0.37	0.39	0.23	0.25	-0.04	4	0.4	0.52	0.07	0.03	0.35	0.35***	4	0.62	0.61	0.08	0.04	0.14	0.01
PaB11[d]	4	0.38	0.41	0.62	0.45	0.50	0.05	4	0.22	0.31	0.17	0.15	0.48	0.38***	4	0.58	0.62	-0.05	-0.04	0.24	0.09
PaB12[d]	15	0.52	0.65	0.83	0.35	0.48	0.22**	24	0.51	0.78	0.65	0.14	0.46	0.41***	20	0.88	0.92	0.02	-0.01	0.15	0.04**
PaC05[d]	6	0.42	0.41	0.39	0.26	0.26	-0.04	12	0.56	0.73	0.64	0.16	0.41	0.30***	7	0.86	0.83	-0.09	-0.02	0.08	-0.05*
PaD07[d]	6	0.30	0.29	0.79	0.70	0.67	-0.04	6	0.39	0.35	0.79	0.54	0.50	-0.10	6	0.79	0.58	0.00	0.01	-0.23	-0.40
PaZ01[d]	12	0.42	0.58	0.85	0.34	0.57	0.28**	12	0.48	0.51	0.86	0.44	0.57	0.09***	7	0.63	0.69	0.34	0.09	0.38	-0.01***

Departures of within-population inbreeding coefficients (F_{IS}) from HWE are indicated by asterisks: *$P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. [a]Microsatellite markers isolated by Boneh *et al.* (2003); [b]Markers isolated by Palma-Silva *et al.* (2007); [c] Markers isolated by Palma-Silva *et al.* (2007); [d]Markers isolated by Paggi *et al.* (2008).

Supplementary Table 3. Analysis of Molecular Variance (AMOVA) based on nuclear microsatellite data for *P. staminea* and *P. albiflos* for two different hierarchical models. **A**, species level. **B**, geographical level (inland *vs.* coastal inselbergs). Percentages of variation in parentheses refer to models in which hybrids were nested with *P. albiflos*.

		Nuclear Microsatellites		
	Source of variation	**Variation %**	***F*-statistics**	***P* - value**
(A) *Taxomonic level*				
Two species *(P. staminea* vs. *P. albiflos)*				
	among species	22 (17)	FCT = 0.220	< 0.001
	Among populations within species	24 (26)	FSC = 0.315	< 0.001
	within populations	53 (57)	FST = 0.466	< 0.001
(B) *Geographic level*				
Inland x Coastal (COR, GRU, NHA vs. CHA, PA, IMB, ITA, ANDO)	among groups	1(1)	FCT = 0.012	n.s.
	Among populations within groups	40(38)	FSC = 0.406	< 0.001
	within populations	59(61)	FST = 0.413	< 0.001

Supplementary Table 4. Genetic divergence (F_{ST}; below diagonal) and gene flow (N_em; above diagonal) for pairs of populations of the inselberg bromeliads *Pitcairnia albiflos* and *P. staminea* and their hybrids. $N_em = (1/ F_{ST} - 1) / 4$

F_{ST} / N_em	alb-CHA	alb -COR	alb -GRU	alb -IMB	alb -PAO	sta-ANDO	sta -CHA	sta -ITA	sta -PAO	hyb-CHA	hyb-PAO
alb-CHA	-	0.60	0.25	0.69	2.07	0.26	0.25	0.33	0.30	1.58	1.34
alb-COR	0.294	-	0.23	0.58	0.66	0.25	0.21	0.32	0.28	0.57	0.69
alb-GRU	0.503	0.519	-	0.41	0.35	0.22	0.19	0.28	0.27	0.29	0.50
alb-IMB	0.267	0.303	0.376	-	0.85	0.37	0.30	0.43	0.39	0.81	1.08
alb-PAO	0.108	0.274	0.419	0.227	-	0.30	0.30	0.37	0.36	1.25	1.96
sta-ANDO	0.492	0.504	0.528	0.405	0.456	-	0.31	1.73	0.53	0.42	0.54
sta CHA	0.504	0.549	0.573	0.450	0.453	0.444	-	0.42	0.85	0.83	0.71
sta-ITA	0.427	0.441	0.468	0.367	0.406	0.126	0.372	-	0.63	0.61	0.69
sta-PAO	0.453	0.472	0.484	0.390	0.407	0.319	0.228	0.283	-	0.74	1.14
hyb-CHA	0.136	0.303	0.460	0.235	0.167	0.374	0.231	0.289	0.253	-	3.83
hyb-PAO	0.157	0.265	0.335	0.188	0.113	0.317	0.262	0.266	0.180	0.061	-

All F_{ST} values were significant at the 0.001 level.

Supplementary Table 5. Locus-specific, bidirectional introgression rates between *Pitcairnia albiflos* and *P. staminea* on PAO population.

Locus	***P. staminea* → *P. albiflos***	***P. albiflos* → *P. staminea***
pit5	42.317	0.000*
pit8	1.160	0.000*
pit9	0.573	1.179
E6b	0.215	0.104
ct5	1.959	1.938
e19	2.976	3.342
VgA04	0.102	0.214
PaA05	1.703	1.906
PaA09	1.623	1.791
PaA10	0.227	0.127
PaB11	2.251	2.187
PaB12	0.355	0.199
PaC05	0.100	0.000
PaD07	0.177	0.000
PaZ01	0.898	0.509

*Strongly asymmetric gene flow